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☐ 1: BA000043. Reports *Geobacillus kaust...*[gi:56378377]

Links

Features Sequence

LOCUS BA000043 1137 bp DNA linear BCT 04-DEC-2004
 DEFINITION *Geobacillus kaustophilus* HTA426 DNA, complete genome.
 ACCESSION BA000043 REGION: 1613..2749
 VERSION BA000043.1 GI:56378377
 KEYWORDS .
 SOURCE *Geobacillus kaustophilus* HTA426
 ORGANISM *Geobacillus kaustophilus* HTA426
 Bacteria; Firmicutes; Bacillales; Bacillaceae; *Geobacillus*.
 REFERENCE 1
 AUTHORS Takami,H., Takaki,Y., Chee,G.J., Nishi,S., Shimamura,S., Suzuki,H.,
 Matsui,S. and Uchiyama,I.
 TITLE Thermoadaptation trait revealed by the genome sequence of
 thermophilic *Geobacillus kaustophilus*
 JOURNAL (er) Nucleic Acids Res. 32 (21), 6292-6303 (2004)
 PUBMED 15576355
 REFERENCE 2 (bases 1 to 1137)
 AUTHORS Takami,H., Takaki,Y. and Chee,G.
 TITLE Direct Submission
 JOURNAL Submitted (25-JUN-2003) Hideto Takami, Japan Marine Science and
 Technology Center, Microbial Genome Analysis Research Group; 2-15
 Natsushima-cho, Yokosuka, Kanagawa 237-0061, Japan
 (E-mail:takamih@jamstec.go.jp,
 URL:http://www.jamstec.go.jp/jamstec-e/bic/exbase.html,
 Tel:81-46-867-9643, Fax:81-46-867-9645)
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1: NC_006274. Reports *Bacillus cereus* E...[gi:52140164]

Links

Comment Features Sequence

LOCUS NC_006274 1140 bp DNA linear BCT 03-DEC-2005
 DEFINITION *Bacillus cereus* E33L, complete genome.
 ACCESSION NC_006274 REGION: 1927..3066
 VERSION NC_006274.1 GI:52140164
 PROJECT GenomeProject:12468
 KEYWORDS .
 SOURCE *Bacillus cereus* E33L
 ORGANISM *Bacillus cereus* E33L
 Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*; *Bacillus cereus* group.
 REFERENCE 1 (bases 1 to 1140)
 AUTHORS Brettin,T.S., Bruce,D., Challacombe,J.F., Gilna,P., Han,C., Hill,K., Hitchcock,P., Jackson,P., Keim,P., Longmire,J., Lucas,S., Okinaka,R., Richardson,P., Rubin,E. and Tice,H.
 TITLE Complete genome sequence of *Bacillus cereus* E33L
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1140)
 CONSRM NCBI Genome Project
 TITLE Direct Submission
 JOURNAL Submitted (16-SEP-2004) National Center for Biotechnology Information, NIH, Bethesda, MD 20894, USA
 REFERENCE 3 (bases 1 to 1140)
 AUTHORS Brettin,T.S., Bruce,D., Challacombe,J.F., Gilna,P., Han,C., Hill,K., Hitchcock,P., Jackson,P., Keim,P., Longmire,J., Lucas,S., Okinaka,R., Richardson,P., Rubin,E. and Tice,H.
 TITLE Direct Submission
 JOURNAL Submitted (14-JUL-2004) Joint Genome Institute, Department of Energy, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final NCBI review. The reference sequence was derived from CP000001.
 COMPLETENESS: full length.
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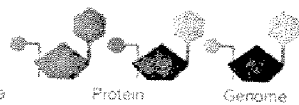
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☐ 1: NC_005957. Reports *Bacillus thuringi...*[gi:49476684]

Links

Comment Features Sequence

LOCUS NC_005957 1140 bp DNA linear BCT 03-APR-2006

DEFINITION *Bacillus thuringiensis* serovar konkukian str. 97-27, complete genome.

ACCESSION NC_005957 REGION: 1928..3067

VERSION NC_005957.1 GI:49476684

PROJECT GenomeProject:10877

KEYWORDS

SOURCE *Bacillus thuringiensis* serovar konkukian str. 97-27

ORGANISM *Bacillus thuringiensis* serovar konkukian str. 97-27
Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*; *Bacillus cereus* group.

REFERENCE 1 (bases 1 to 1140)

AUTHORS Brettin,T.S., Bruce,D., Challacombe,J.F., Gilna,P., Han,C., Hill,K., Hitchcock,P., Jackson,P., Keim,P., Longmire,J., Lucas,S., Okinaka,R., Richardson,P., Rubin,E. and Tice,H.

TITLE Complete genome sequence of *Bacillus thuringiensis* 97-27

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1140)

CONSRM NCBI Genome Project

TITLE Direct Submission

JOURNAL Submitted (11-SEP-2004) National Center for Biotechnology Information, NIH, Bethesda, MD 20894, USA

REFERENCE 3 (bases 1 to 1140)

AUTHORS Brettin,T.S., Bruce,D., Challacombe,J.F., Gilna,P., Han,C., Hill,K., Hitchcock,P., Jackson,P., Keim,P., Longmire,J., Lucas,S., Okinaka,R., Richardson,P., Rubin,E. and Tice,H.

TITLE Direct Submission

JOURNAL Submitted (07-JUN-2004) Joint Genome Institute, Department of Energy, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final NCBI review. The reference sequence was derived from AE017355. *Bacillus thuringiensis* 97-27 (subsp. konkukian (serotype H34)) was originally isolated from a case of severe human tissue necrosis (*Bacillus thuringiensis* subsp. konkukian (serotype H34) superinfection: Case report and experimental evidence of pathogenicity in immunosuppressed mice. Hernandez, E, Ramisse, F, Ducoureaux, J-P, Cruel, T, and Cavallo, J-D. J Clin Microbiol 1998 36(7):2138-2139). *B. thuringiensis* is indigenous to many habitats worldwide; these include soil, insects, deciduous and coniferous leaves (Prediction of insecticidal activity of *Bacillus thuringiensis* strains by polymerase chain reaction product profiles. Carozzi, NB, Kramer, VC, Warren, GW, Evola, S, and Koziel, MG. Appl Environ Microbiol. 1991 57(11):3057-61). *B. thuringiensis* is an insect pathogen that is widely used as a biopesticide in commercial agriculture. Infection of humans is unusual. The apparent pathogenic properties of *B. thuringiensis* 97-27 are very unusual for *B. thuringiensis*; unlike most *B.*

thuringiensis isolates, this isolate is very closely related to *B. anthracis* based on phylogenetic analysis (Fluorescent amplified fragment length polymorphism analysis of *Bacillus anthracis*, *Bacillus cereus*, and *Bacillus thuringiensis* isolates. Hill, KK, Ticknor, LO, Okinaka, RT, Asay, M, Blair, H, Bliss, KA, Laker, M, Pardington, PE, Richardson, AP, Tonks, M, Beecher, DJ, Kemp, JD, Kolsto, A-B, Wong, ACL, Keim, P, and Jackson, PJ. Appl Environ Microbiol 70(2):1068-1080. Plasmid and fosmid libraries were prepared at the Joint Genome Institute in Los Alamos (JGI-LANL), NM. Shotgun sequencing was performed at the JGI Production Genomics Facility (JGI-PGF) in Walnut Creek, CA to a coverage of 24x. Finishing was performed at JGI-LANL starting with 83 contigs and 16 scaffolds. Repetitive regions were identified, assembled and finished by manually checking paired reads close to each repeat in the assembly with consed and then making a subassembly for each repetitive region. Fifty five gaps were closed with primer walks and 16 by PCR. Gene predictions were obtained using Glimmer and tRNAs were identified using tRNAscan-SE. Basic analysis of the gene predictions was performed by comparing coding sequences against the PFam, BLOCKS and Prodom databases. Gene definitions and functional classes were added manually by a team of annotators at JGI-LANL, using BLAST results in addition to information from the basic analysis. A total of 5540 features have been annotated on the sequence record.

COMPLETENESS: full length.

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ORIGIN
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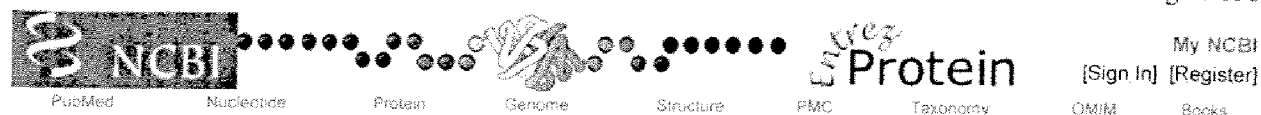
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☐ 1: EAR74115. Reports DNA polymerase III...[gi:89154071]BLink, Conserved
Domains, Links

Comment Features Sequence

LOCUS EAR74115 381 aa linear BCT 03-MAR-2006
DEFINITION DNA polymerase III, beta chain [Bacillus weihenstephanensis KBAB4].
ACCESSION EAR74115
VERSION EAR74115.1 GI:89154071
DBSOURCE accession [AA0Y01000054.1](#)
KEYWORDS .
SOURCE Bacillus weihenstephanensis KBAB4
ORGANISM [Bacillus weihenstephanensis KBAB4](#)
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE 1 (residues 1 to 381)
AUTHORS Lapidus,A., Goltsman,E., Copeland,A., Lucas,S., Barry,K.,
Detter,J.C., Glavina del Rio,T., Hammon,N., Israni,S., Dalin,E.,
Tice,H., Bruce,D., Pitluck,S., Richardson,P., Auger,S.,
Galleron,N., Sanchis,V., Gohar,M., Broussole,V., Brillard,J.,
Guinebretiere,M.-H., Ehrlich,S.D., Lereclus,D., Aymerich,S.,
Nguen-the,C. and Sorokin,A.
CONSRTM US DOE Joint Genome Institute (JGI-PGF)
TITLE Sequencing of the draft genome and assembly of Bacillus
weihenstephanensis KBAB4
JOURNAL Unpublished

REFERENCE 2 (residues 1 to 381)
AUTHORS Larimer,F. and Land,M.
CONSRTM US DOE Joint Genome Institute (JGI-ORNL)
TITLE Annotation of the draft genome assembly of Bacillus
weihenstephanensis KBAB4
JOURNAL Unpublished

REFERENCE 3 (residues 1 to 381)
AUTHORS Lapidus,A., Goltsman,E., Copeland,A., Lucas,S., Barry,K.,
Detter,J.C., Glavina del Rio,T., Hammon,N., Israni,S., Dalin,E.,
Tice,H., Bruce,D., Pitluck,S., Richardson,P., Auger,S.,
Galleron,N., Sanchis,V., Gohar,M., Broussole,V., Brillard,J.,
Guinebretiere,M.-H., Ehrlich,S.D., Lereclus,D., Aymerich,S.,
Nguen-the,C. and Sorokin,A.
CONSRTM US DOE Joint Genome Institute (JGI-PGF)
TITLE Direct Submission
JOURNAL Submitted (02-MAR-2006) US DOE Joint Genome Institute, 2800
Mitchell Drive B100, Walnut Creek, CA 94598-1698, USA

COMMENT URL -- <http://www.jgi.doe.gov>
Contact: Paul Richardson (microbes@cuba.jgi-psf.org)
Draft sequencing done at US DOE Joint Genome Institute
Source DNA and bacteria available from Alexei Sorokin
(alexei.sorokine@jouy.inra.fr)
The JGI and collaborators endorse the principles for the
distribution and use of large scale sequencing data adopted by the
larger genome sequencing community and urge users of this data to

follow them. It is our intention to publish the work of this project in a timely fashion and we welcome collaborative interaction on the project and analysis.

(<http://www.genome.gov/page.cfm?pageID=10506376>)

Notes:

Bacillus weihenstephanensis KBAB4 was originally isolated from forest soil near Versailles, France, and was originally identified as *Bacillus cereus* (Vilas-Boas et al, Appl Env Microbiol, 2002, 68, 1414). More detailed phylogenetic analysis, using MLST, of the Versailles Collection of *B. cereus* and *B. thuringiensis* strains revealed that the strain grows at low temperature (60C) and clusters with many other strains able to grow at low temperatures, including the independently isolated and characterized strains WSBC10204 and WSBC10206 (Sorokin et al, Appl Env Microbiol, 2006, 72, 1569). The latter two strains are the type strains of a newly recognized species in the *B. cereus* group able to grow in cold and having the species name *Bacillus weihenstephanensis* (Lechner et al, Int. J. Syst. Bacteriol, 1998, 48, 1373). Since, by MLST, KBAB4 is very closely related to WSBC10204 and represents many other psychrotrophic strains, it was assigned a species name *Bacillus weihenstephanensis* and the strain KBAB4 should also be considered as a type representative of this species.

Method: conceptual translation.

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☐ 1: NC_000964. Reports *Bacillus subtilis*...[gi:50812173]

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LOCUS NC_000964 1137 bp DNA linear BCT 02-DEC-2005

DEFINITION *Bacillus subtilis* subsp. *subtilis* str. 168, complete genome.

ACCESSION NC_000964 REGION: 1939..3075

VERSION NC_000964.2 GI:50812173

PROJECT GenomeProject:76

KEYWORDS complete genome.

SOURCE *Bacillus subtilis* subsp. *subtilis* str. 168

ORGANISM *Bacillus subtilis* subsp. *subtilis* str. 168
Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.

REFERENCE 1 (bases 1 to 1137)

AUTHORS Kunst, F., Ogasawara, N., Moszer, I., Albertini, A.M., Alloni, G., Azevedo, V., Bertero, M.G., Bessieres, P., Bolotin, A., Borchert, S., Borris, R., Boursier, L., Brans, A., Braun, M., Brignell, S.C., Bron, S., Brouillet, S., Bruschi, C.V., Caldwell, B., Capuano, V., Carter, N.M., Choi, S.K., Codani, J.J., Connerton, I.F., Cummings, N.J., Daniel, R.A., Denizot, F., Devine, K.M., Dusterhoft, A., Ehrlich, S.D., Emmerson, P.T., Entian, K.D., Errington, J., Fabret, C., Ferrari, E., Foulger, D., Fritz, C., Fujita, M., Fujita, Y., Fuma, S., Galizzi, A., Galleron, N., Ghim, S.Y., Glaser, P., Goffeau, A., Golightly, E.J., Grandi, G., Guiseppe, G., Guy, B.J., Haga, K., Halech, J., Harwood, C.R., Henaut, A., Hilbert, H., Holsappel, S., Hosono, S., Hullo, M.F., Itaya, M., Jones, L., Joris, B., Karamata, D., Kasahara, Y., Klaerr-Blanchard, M., Klein, C., Kobayashi, Y., Koetter, P., Koningstein, G., Krogh, S., Kumano, M., Kurita, K., Lapidus, A., Lardinois, S., Lauber, J., Lazarevic, V., Lee, S.M., Levine, A., Liu, H., Masuda, S., Mauel, C., Medigue, C., Medina, N., Mellado, R.P., Mizuno, M., Moestl, D., Nakai, S., Noback, M., Noone, D., O'Reilly, M., Ogawa, K., Ogiwara, A., Oudega, B., Park, S.H., Parro, V., Pohl, T.M., Portetelle, D., Porwollik, S., Prescott, A.M., Presecan, E., Pujic, P., Purnelle, B., Rapoport, G., Rey, M., Reynolds, S., Rieger, M., Rivolta, C., Rocha, E., Roche, B., Rose, M., Sadaie, Y., Sato, T., Scanlan, E., Schleich, S., Schroeter, R., Scoffone, F., Sekiguchi, J., Sekowska, A., Seror, S.J., Serror, P., Shin, B.S., Soldo, B., Sorokin, A., Tacconi, E., Takagi, T., Takahashi, H., Takemaru, K., Takeuchi, M., Tamakoshi, A., Tanaka, T., Terpstra, P., Tognoni, A., Tosato, V., Uchiyama, S., Vandenbol, M., Vannier, F., Vassarotti, A., Viari, A., Wambutt, R., Wedler, E., Wedler, H., Weitzenegger, T., Winters, P., Wipat, A., Yamamoto, H., Yamane, K., Yasumoto, K., Yata, K., Yoshida, K., Yoshikawa, H.F., Zumstein, E., Yoshikawa, H. and Danchin, A.

TITLE The complete genome sequence of the gram-positive bacterium *Bacillus subtilis*

JOURNAL Nature 390 (6657), 249-256 (1997)

PUBMED 9384377

REFERENCE 2 (bases 1 to 1137)

CONSRM NCBI Genome Project

TITLE Direct Submission

JOURNAL Submitted (12-OCT-2001) National Center for Biotechnology Information, NIH, Bethesda, MD 20894, USA

REFERENCE 3 (bases 1 to 1137)

AUTHORS Kunst, F., Ogasawara, N., Yoshikawa, H. and Danchin, A.

TITLE Direct Submission

JOURNAL Submitted (18-NOV-1997) Institut Pasteur, Regulation de l'Expression Genetique, 28 rue du Docteur Roux, Paris Cedex 15 75724, France

COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final NCBI review. The reference sequence was derived from AL009126. On Jul 29, 2004 this sequence version replaced gi:16077068. COMPLETENESS: full length.

FEATURES

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ORIGIN

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☐ 1: YP_089686. Reports DNA polymerase III...[gi:52783857]BLink, Conserved
Domains, Links

Comment Features Sequence

LOCUS YP_089686 378 aa linear BCT 03-DEC-2005

DEFINITION DNA polymerase III subunit beta [Bacillus licheniformis ATCC 14580].

ACCESSION YP_089686

VERSION YP_089686.1 GI:52783857

DBSOURCE REFSEQ: accession NC_006322.1

KEYWORDS .

SOURCE Bacillus licheniformis ATCC 14580 (DSM 13)

ORGANISM Bacillus licheniformis ATCC 14580
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

REFERENCE 1 (residues 1 to 378)

AUTHORS Veith,B., Herzberg,C., Steckel,S., Feesche,J., Maurer,K.H., Ehrenreich,P., Baeumer,S., Henne,A., Liesegang,H., Merkl,R., Ehrenreich,A. and Gottschalk,G.

TITLE The complete genome sequence of Bacillus licheniformis DSM13, an organism with great industrial potential

JOURNAL Unpublished

REFERENCE 2 (residues 1 to 378)

CONSRM NCBI Genome Project

TITLE Direct Submission

JOURNAL Submitted (28-SEP-2004) National Center for Biotechnology Information, NIH, Bethesda, MD 20894, USA

REFERENCE 3 (residues 1 to 378)

AUTHORS Veith,B., Herzberg,C., Steckel,S., Feesche,J., Maurer,K.H., Ehrenreich,P., Baeumer,S., Henne,A., Liesegang,H., Merkl,R., Ehrenreich,A. and Gottschalk,G.

TITLE Direct Submission

JOURNAL Submitted (30-APR-2004) Institute of Microbiology and Genetics, Georg August University Goettingen, Goettingen Genomics Laboratory, Grisebachstr. 8, Goettingen D-37077, Germany

COMMENT VALIDATED REFSEQ: This record has undergone preliminary review of the sequence, but has not yet been subject to final review. The reference sequence was derived from AAU38993.
Method: conceptual translation.

FEATURES Location/Qualifiers

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